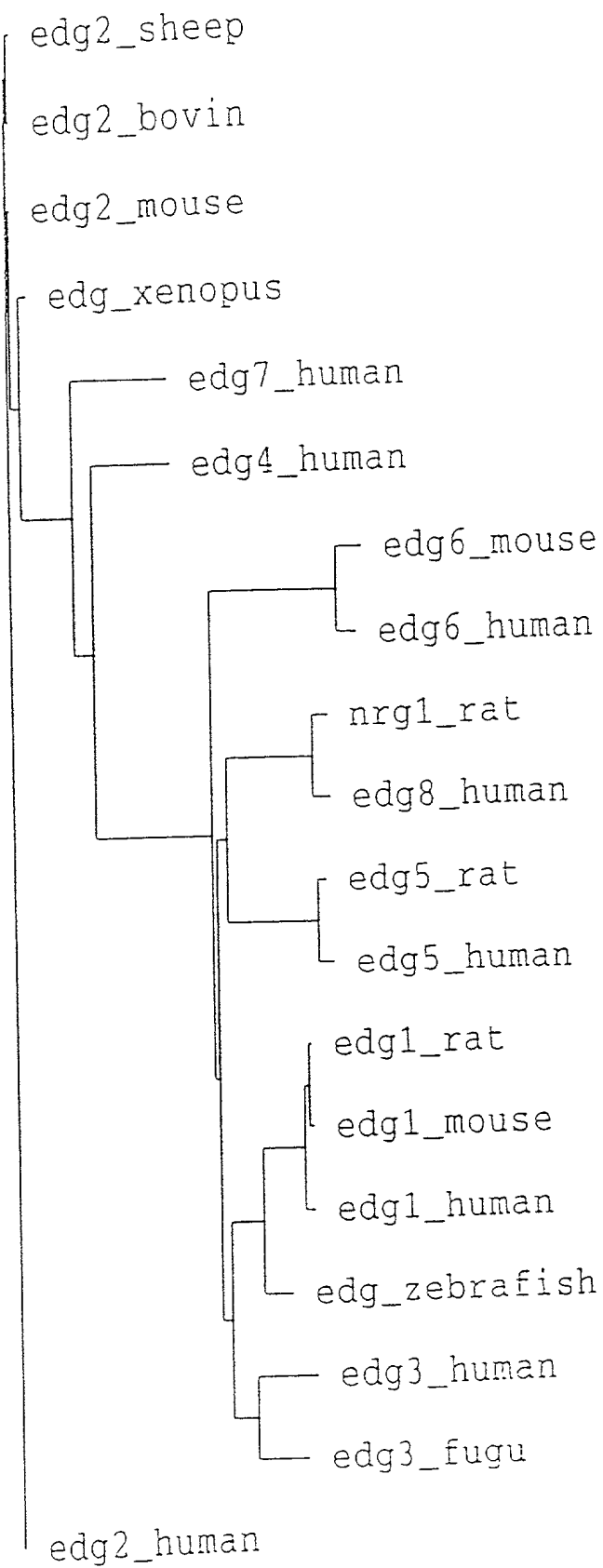


FIG 1A

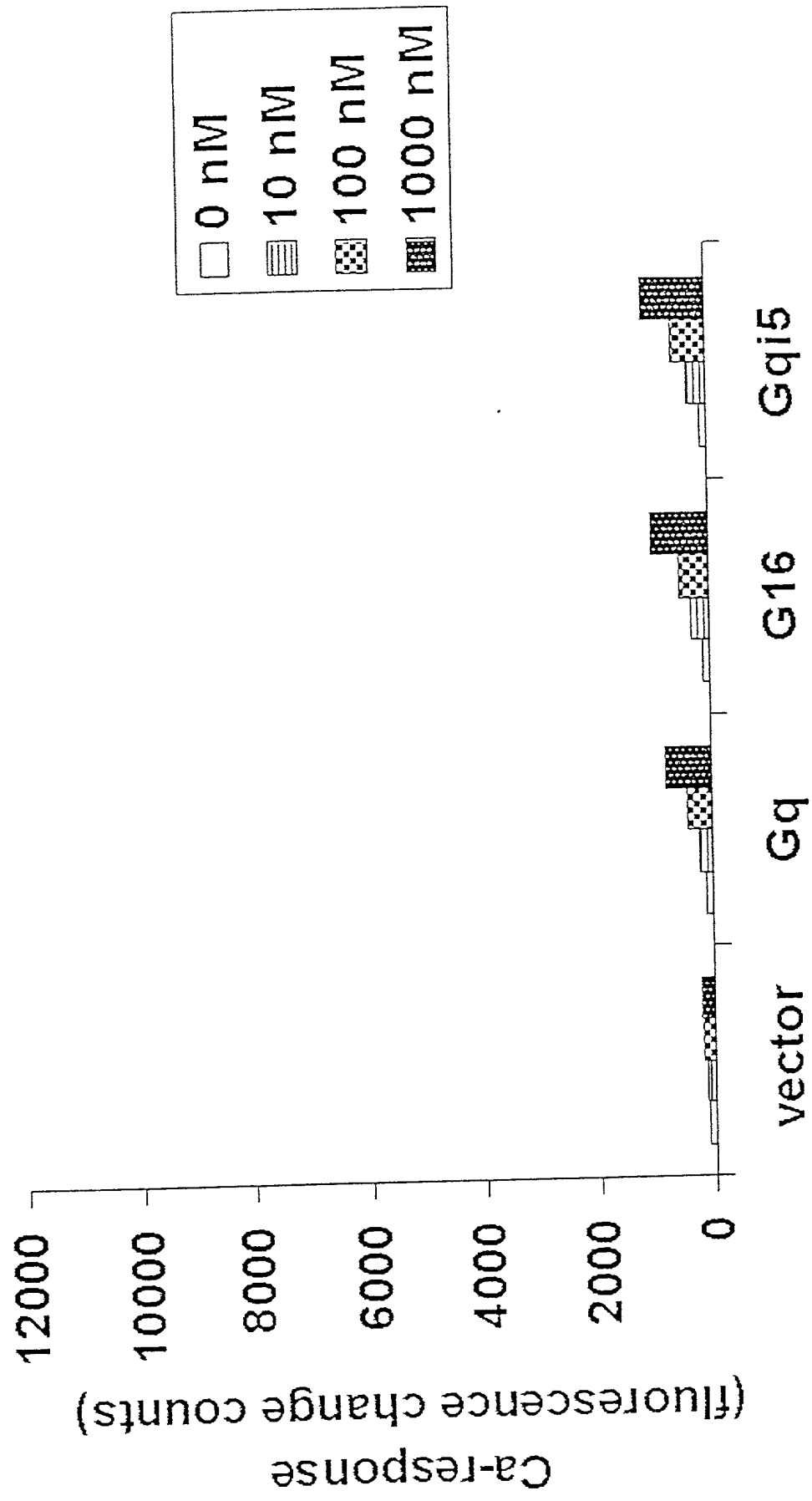
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 M E S G L L R P A P V S E V I V L H Y N
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 Y T G K L R G A R Y Q P G A G L R A D A
 121 GTGGTGTGCCTGGCGGTGTGCGCCTTCATCGTGCTAGAGAATCTAGCCGTGTTGTTGGTG
 V V C L A V C A F I V L E N L A V L L V
 181 CTCGGACGCCACCCGCGCTTCCACGCTCCCATGTTCTGCTCCTGGGCAGCCTCACGTTG
 L G R H P R F H A P M F L L L G S L T L
 241 TCGGATCTGCTGGCAGGCGCCGCTACGCCGCCAACATCCTACTGTGCGGGCCGCTCACG
 S D L L A G A A Y A A N I L L S G P L T
 301 CTGAAACTGTCCCCCGCGCTCTGGTTCGCACGGGAGGGAGGCGTCTTCGTGGCACTCACT
 L K L S P A L W F A R E G G V F V A L T
 361 GCGTCCGTGCTGAGCCTCCTGGCCATCGCGCTGGAGCGCAGCCTCACCATGGCGCGCAGG
 A S V L S L L A I A L E R S L T M A R R
 421 GGGCCCGCGCCCGTCTCCAGTCGGGGGCGCACGCTGGCGATGGCAGCCGCGGCCTGGGGC
 G P A P V S S R G R T L A M A A A A W G
 481 GTGTCGCTGCTCCTCGGGCTCCTGCCAGCGCTGGGCTGGAATTGCCTGGGTGCGCTGGAC
 V S L L L G L L P A L G W N C L G R L D
 541 GCTTGCTCCACTGTCTTGCCGCTCTACGCCAAGGCCTACGTGCTCTTCTGCGTGCTCGCC
 A C S T V L P L Y A K A Y V L F C V L A
 601 TTCGTGGGCATCCTGGCCGCTATCTGTGCACTCTACGCGCGCATCTACTGCCAGGTACGC
 F V G I L A A I C A L Y A R I Y C Q V R
 661 GCCAACGCGCGCGCCTGCCGGCACGGCCCGGGACTGCGGGGACCACCTCGACCCGGGGC
 A N A R R L P A R P G T A G T T S T R A
 721 CGTCGCAAGCCGCGCTCGCTGGCCTTGCTGCGCACGCTCAGCGTGGTGCTCCTGGCCTTT
 R R K P R S L A L L R T L S V V L L A F
 781 GTGGCATGTTGGGGCCCCCTCTTCCTGCTGCTGTTGCTCGACGTGGCGTGCCCGGCGCGC
 V A C W G P L F L L L L L D V A C P A R
 841 ACCTGTCCTGTACTCCTGCAGGCCGATCCCTTCCTGGGACTGGCCATGGCCAACCTCACTT
 T C P V L L Q A D P F L G L A M A N S L
 901 CTGAACCCCATCATCTACACGCTCACCAACCGCGACCTGCGCCACGCGCTCCTGCGCCTG
 L N P I I Y T L T N R D L R H A L L R L
 961 GTCTGCTGCGGACGCCACTCCTGCGGCAGAGACCCGAGTGGCTCCCAGCAGTCGGCGAGC
 V C C G R H S C G R D P S G S Q Q S A S
 1021 GCGGCTGAGGCTTCCGGGGGCTGCGCCGCTGCCTGCCCCGGGCTTGATGGGAGCTTC
 A A E A S G G L R R C L P P G L D G S F
 1081 AGCGGCTCGGAGCGCTCATCGCCCCAGCGCGACGGGCTGGACACCAGCGGCTCCACAGGC
 S G S E R S S P Q R D G L D T S G S T G
 1141 AGCCCCGGTGACCCACAGCCCGCCGACTCTGGTATCAGAACCGGCTGCAGACTGA
 S P G A P T A A R T L V S E P A A D *



	361								418
edg2_human	LNHTILAGVH	SNQHSVV---	-----	-----	-----	-----	-----	-----	
edg7_human	IPSTVLSRSD	TGSQYIEDSI	SQGAVCNKST	S-----	-----	-----	-----	-----	
edg4_human	GASTRIMLPE	NGHPLMTPPF	SYLELQRYAA	SNKSTAPOOL	WVLLAQPNQ	Q-----	-----	-----	
edg1_human	AGFRFRLPIA	GMEFSRSL..	.SDNSSHPQK	DEGDNPETIM	SSGNVNSSS-	-----	-----	-----	
edg3_human	RGARASPIQP	ALOPSRSKSS	SSNSSSHSPK	VKEDLPHTOP	SSCIMDKNAA	LQNGIFCN	-----	-----	
edg5_human	GRRRVGTPGH	HLLPLASSSS	LERGMHMPTS	PTFLLEGNTV	-----	-----	-----	-----	
edg8_human	AAEASGGLR	CLPPGLDGSF	SGSERSSPQR	QGLDTSGSTG	SPGAPTAART	LVSEPAAD	-----	-----	
edg6_human	AHSGASTDSS	SLRP..RSFR	GSRLSFRMR	EPLSSISSYR	SI-----	-----	-----	-----	

Fig. 1C

FIG 2A



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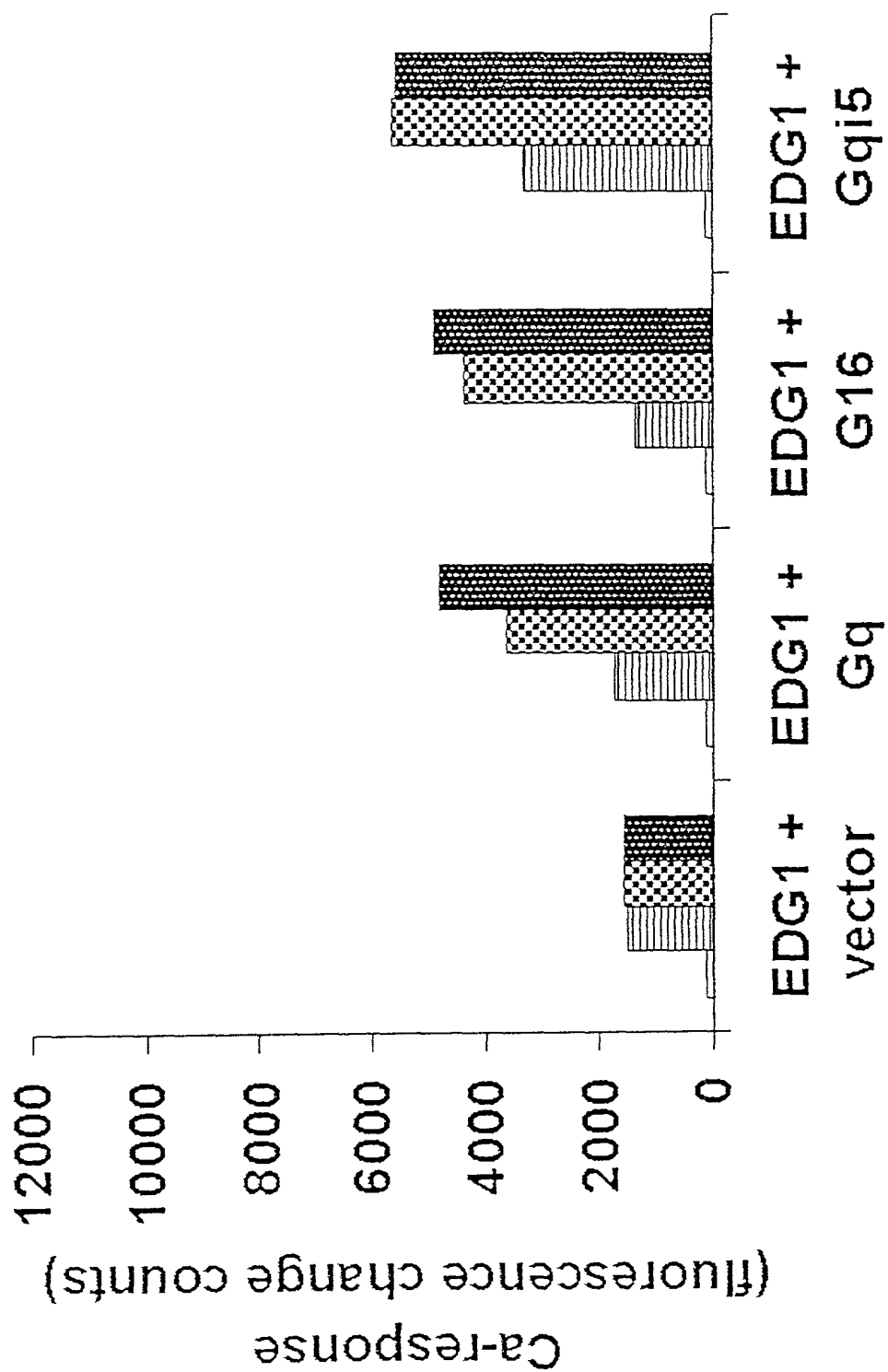


FIG 2C

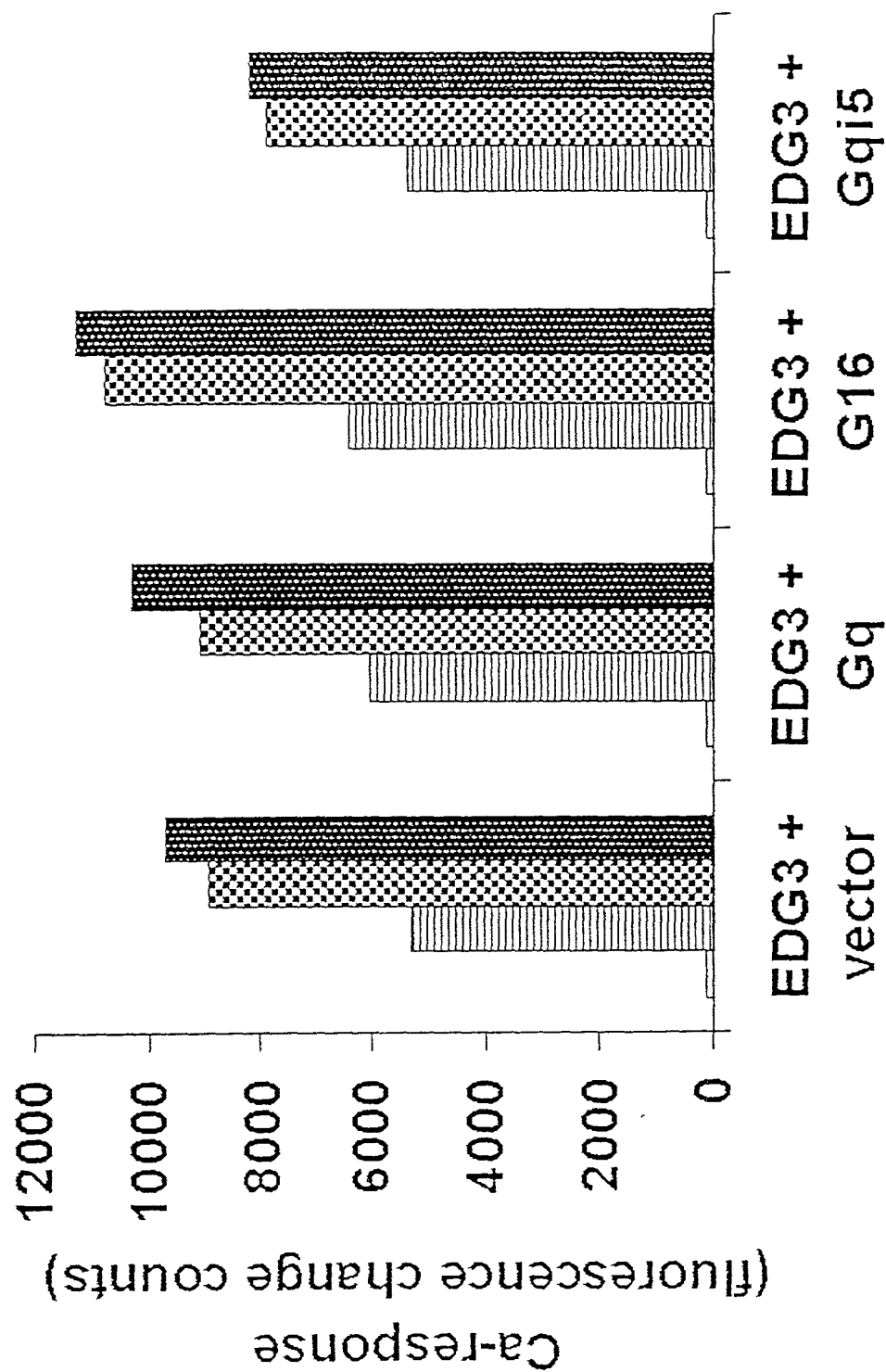
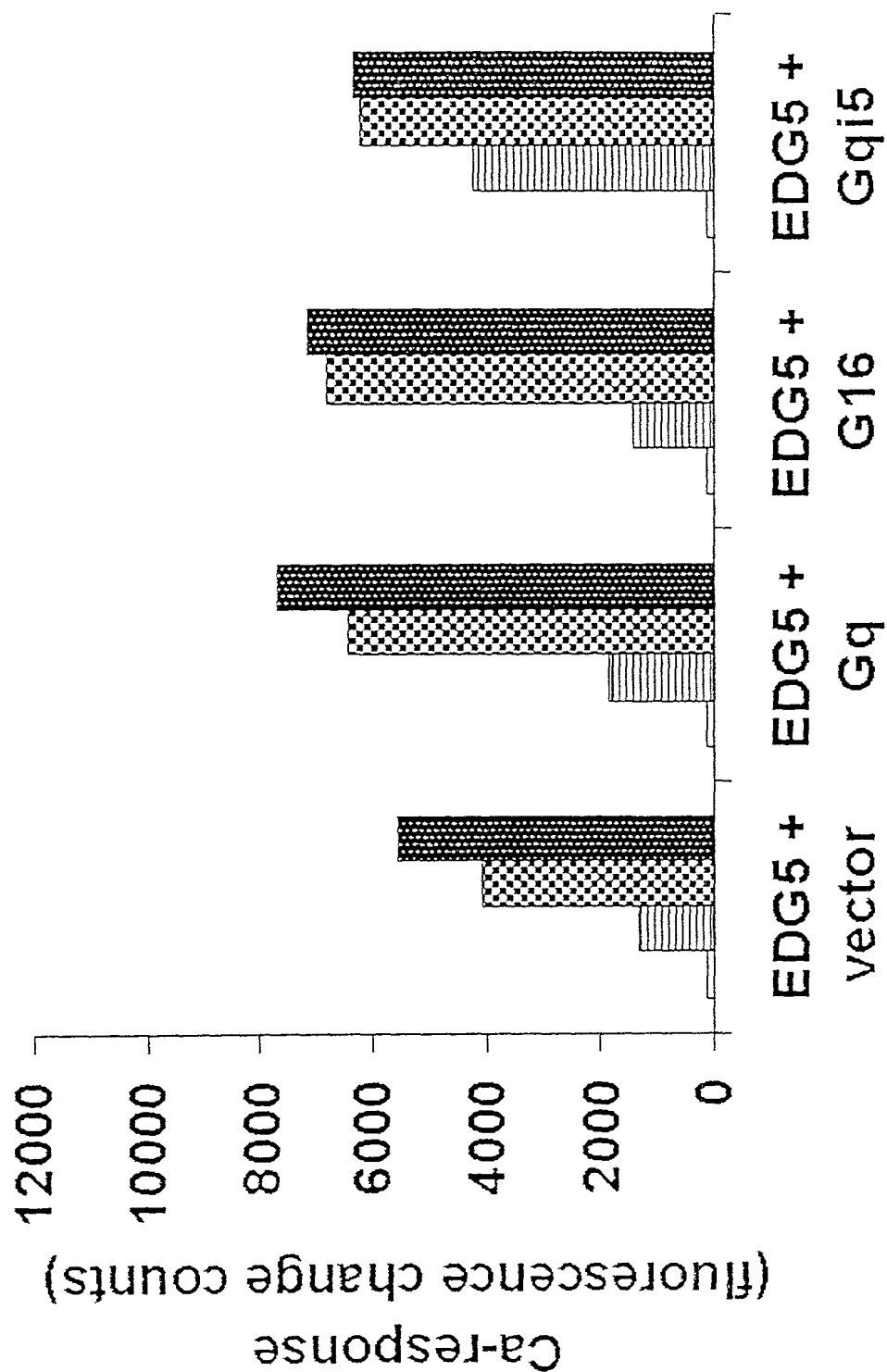
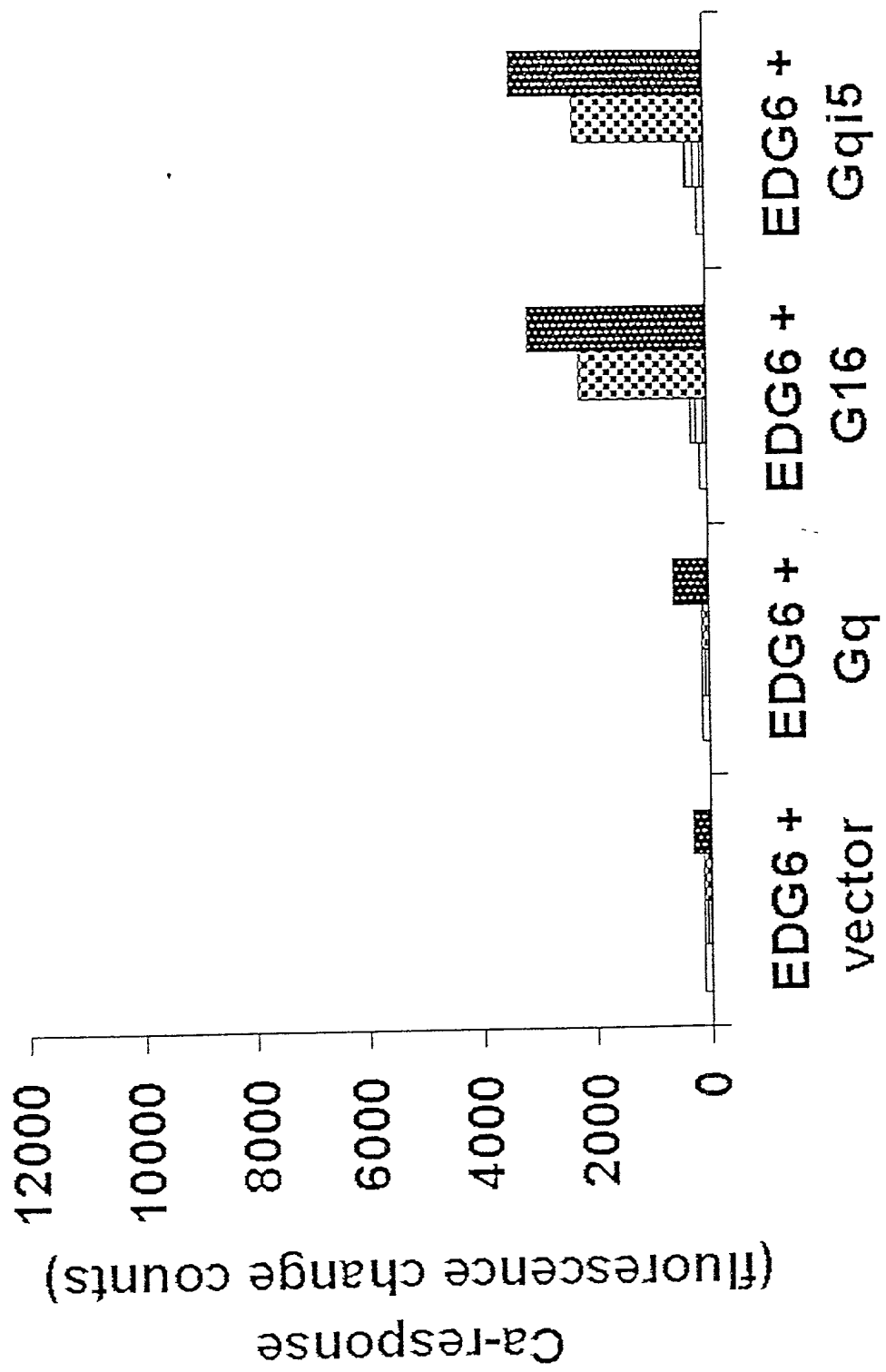


FIG 2D

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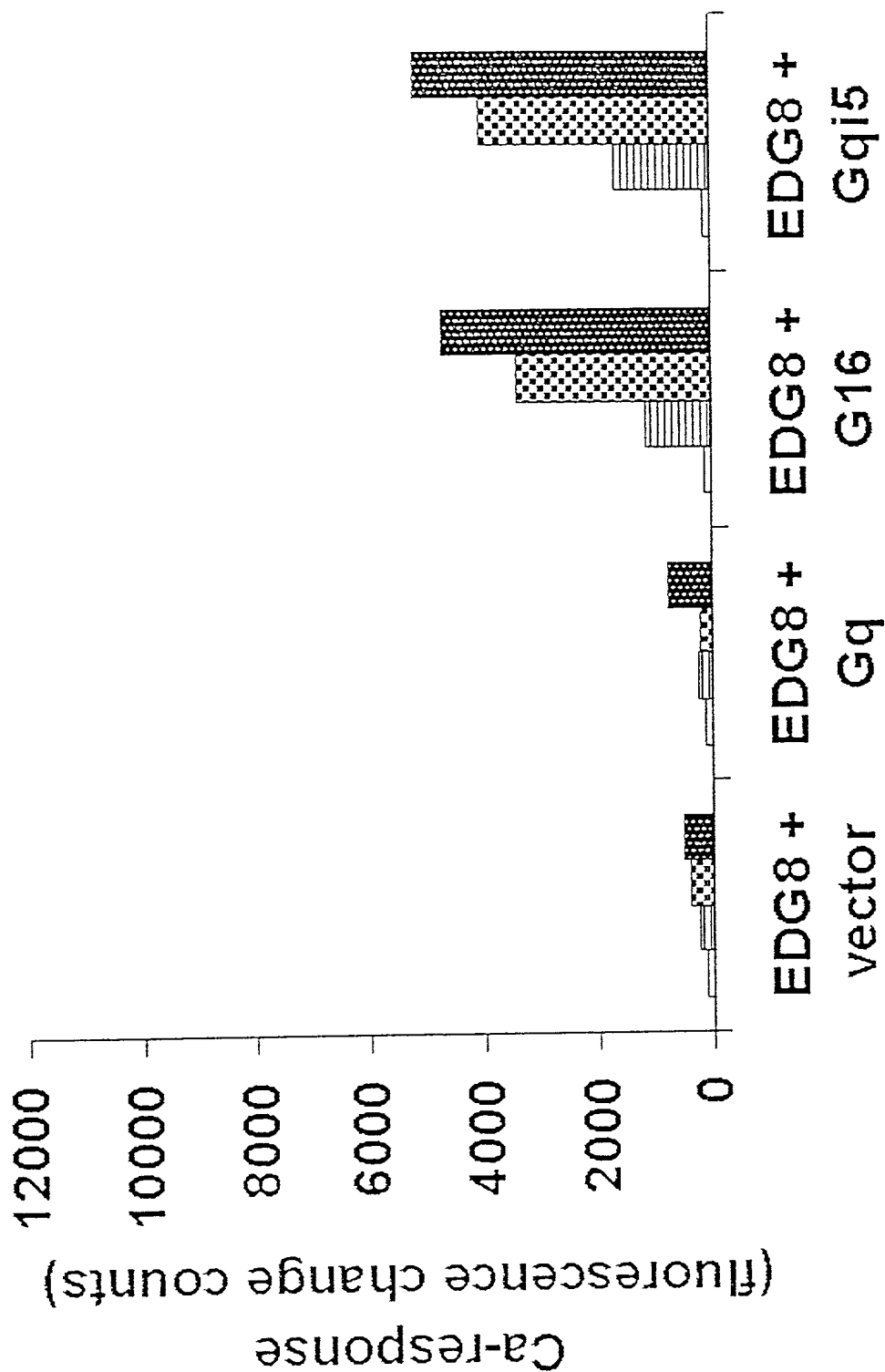


FIG 3

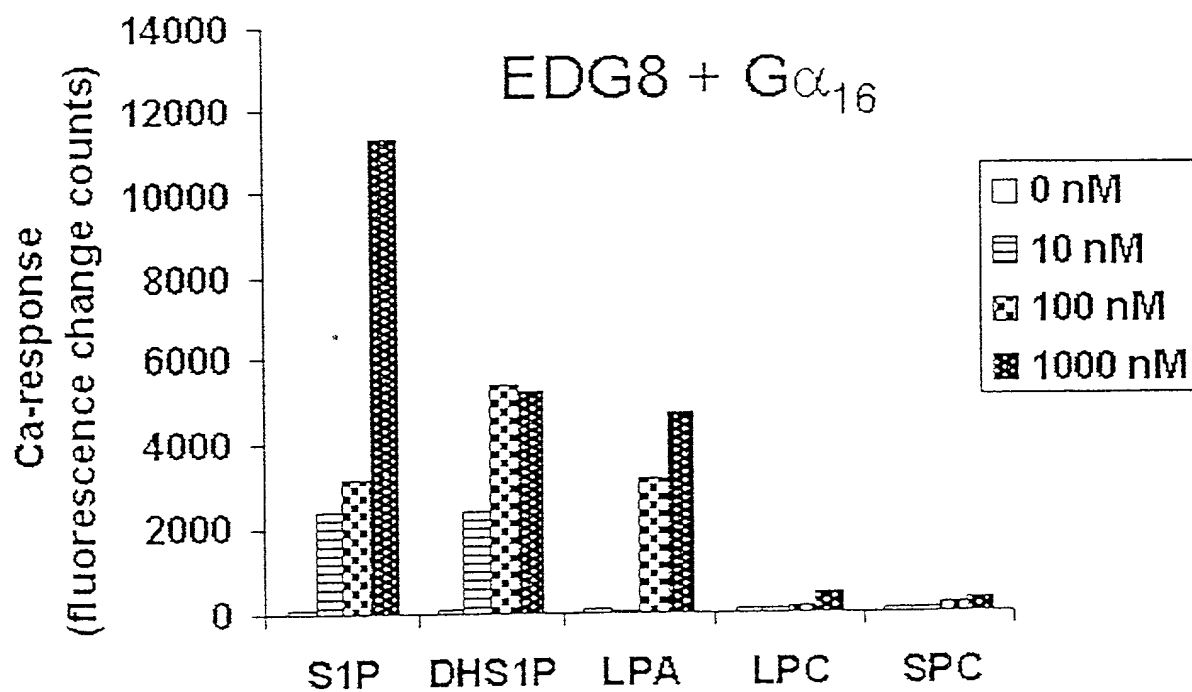
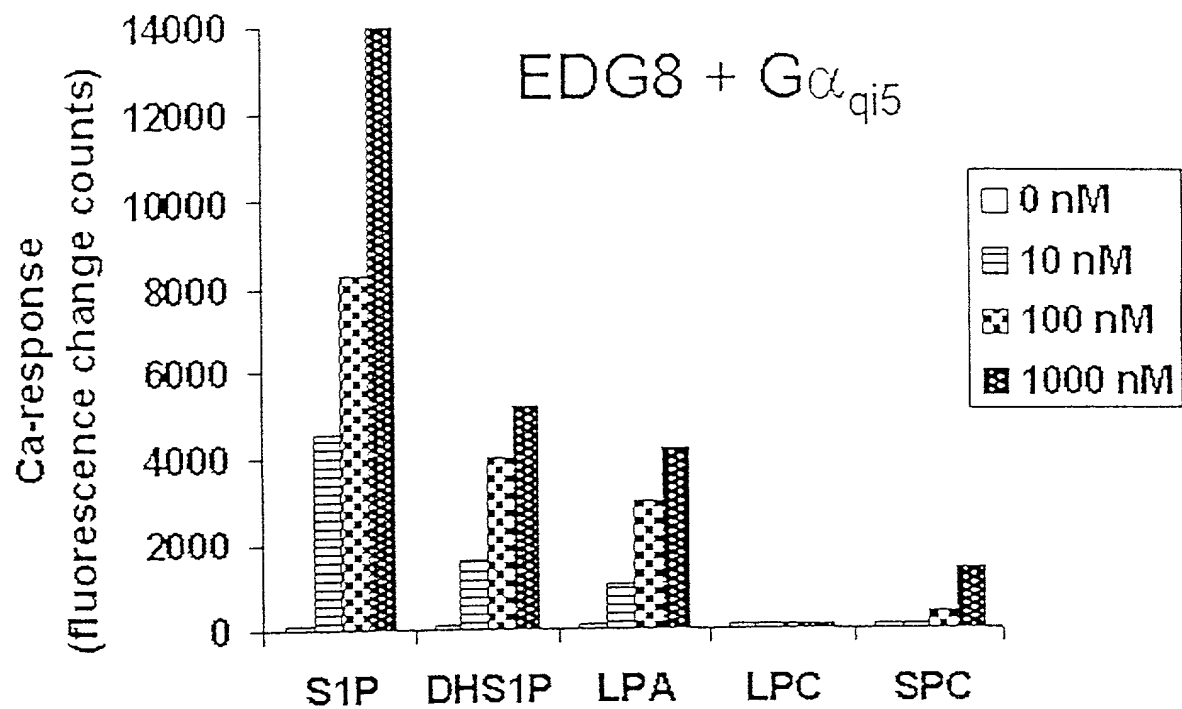
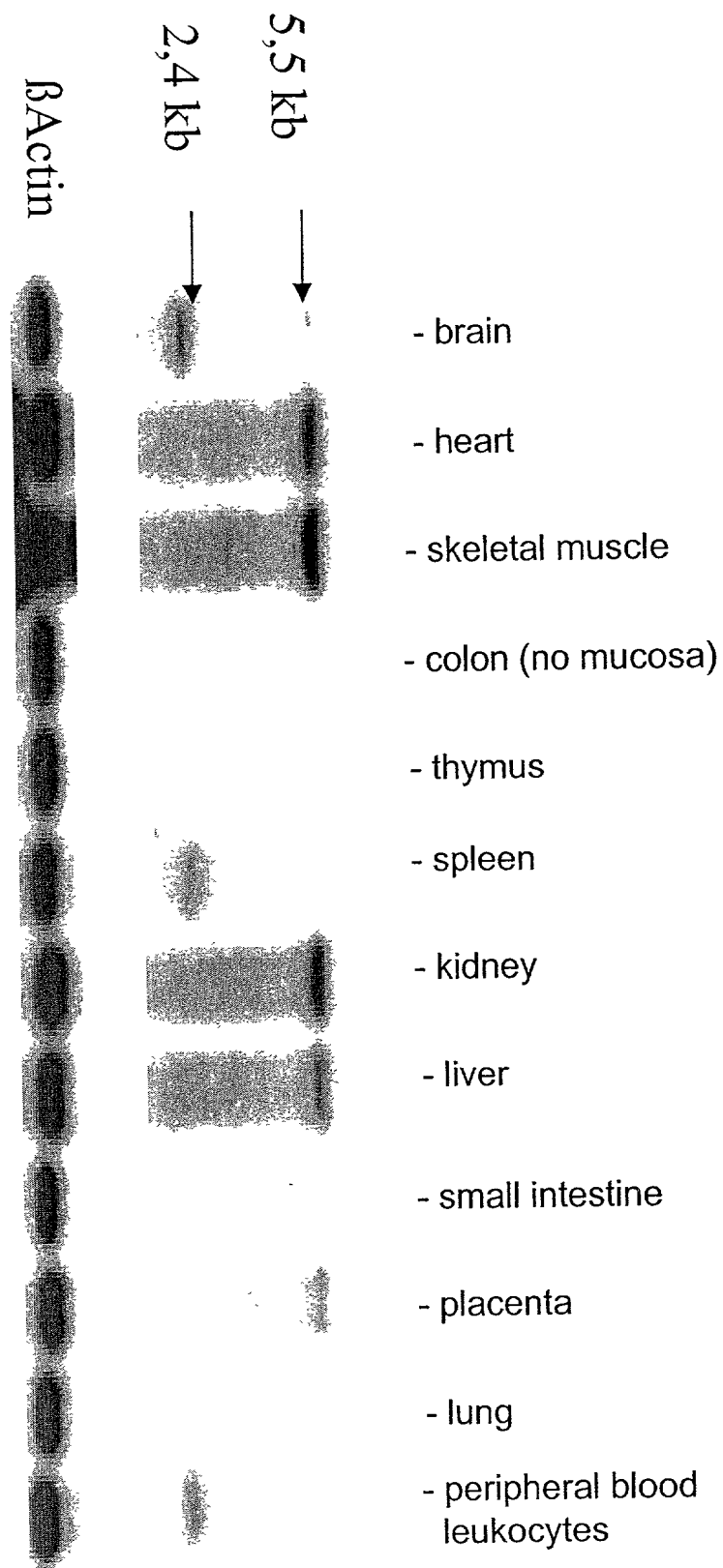


FIG 4

Human EDG8 tissue expression



522 bp 

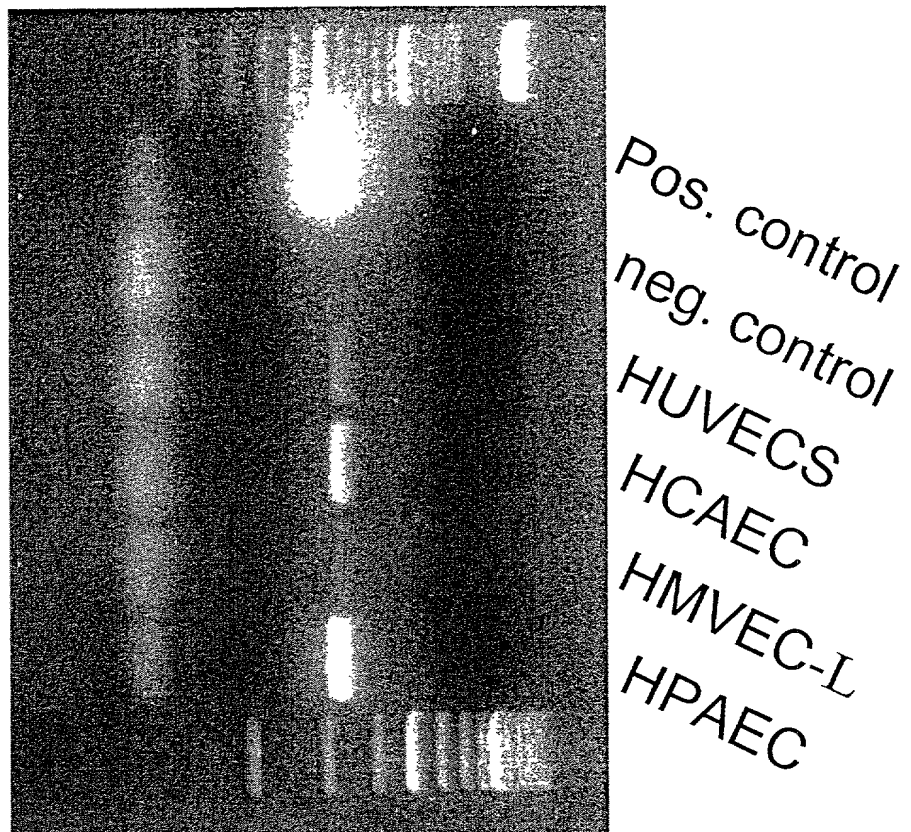


FIG 5B

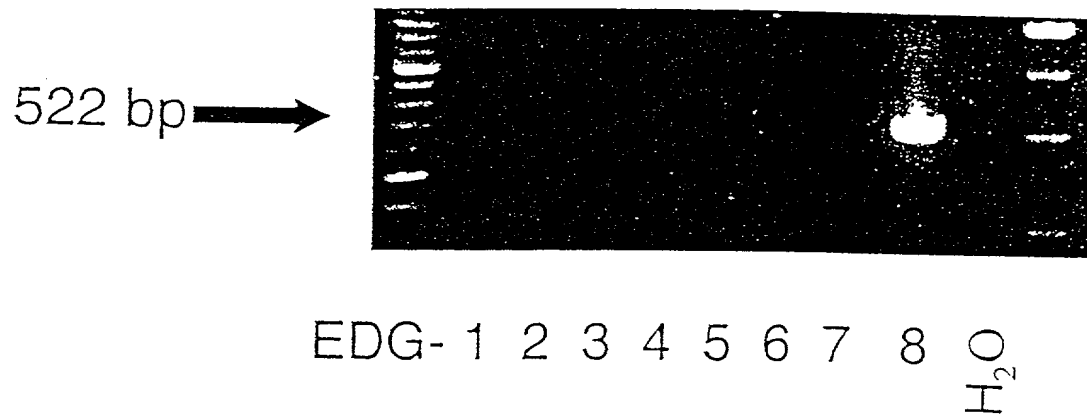
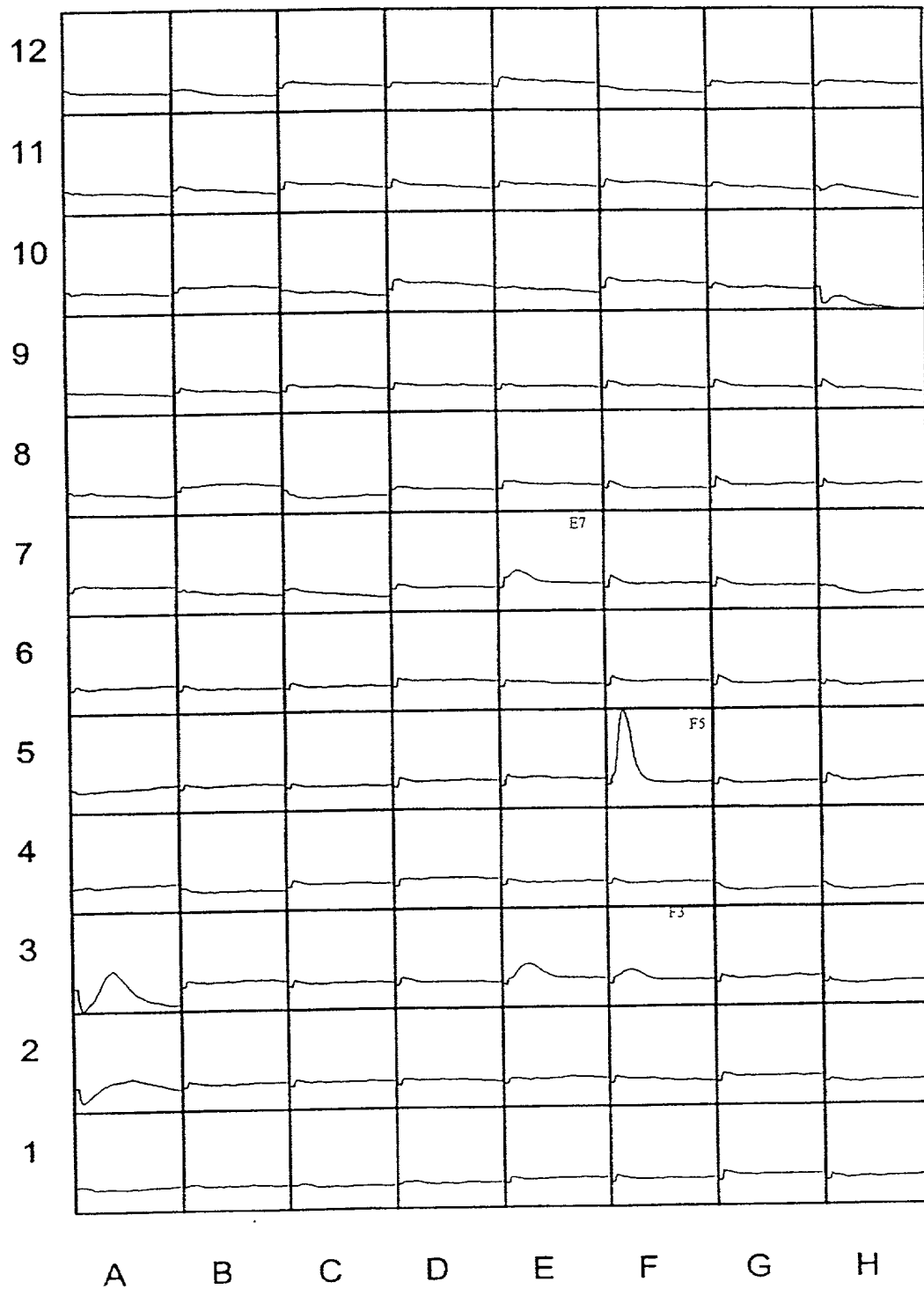


Fig. 6A

qi5 background



rEDG8

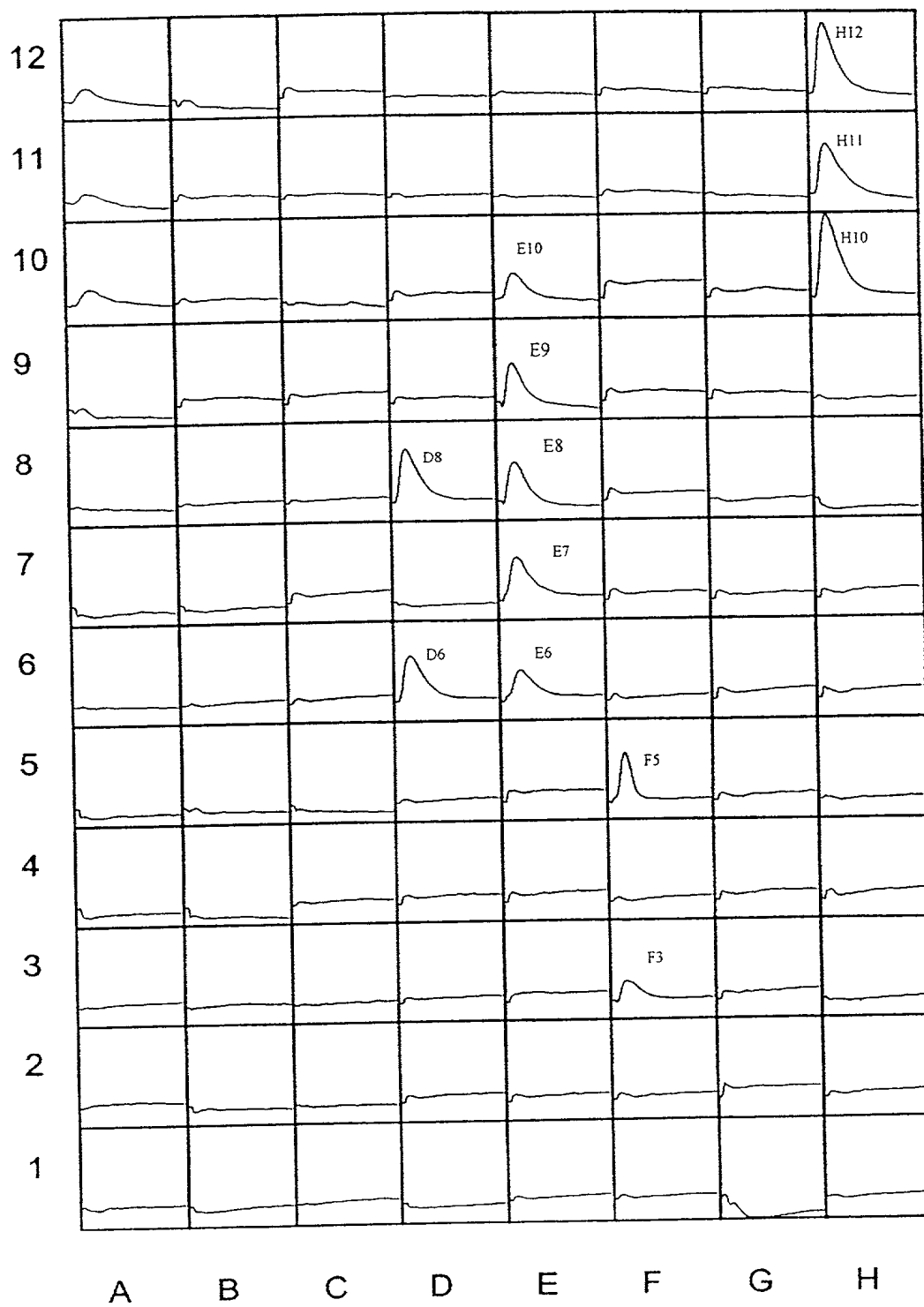


Fig.6C

Fluorescence Change counts

Wells	Lipid	background	rEDG8	stand. response
H10-H12	1 μ M S1P	0	5196	5196
F5	1 μ M LPA	5893	4327	-1566
F3	1 μ M cPAF	1017	1570	553
E10	1 μ M EPA PAF	0	1354	1354
E9	1 μ M AA PAF	0	3121	3121
E8	1 μ M Enantio PAF	0	3883	3883
E7	1 μ M paf C18:1	1256	3765	2509
E6	1 μ M Lyso PAF	0	2421	2421
D8	1 μ M dhS1P	0	5144	5144
D6	1 μ M S1P	0	3672	3672

Fig. 7A

qi5 background in HEK

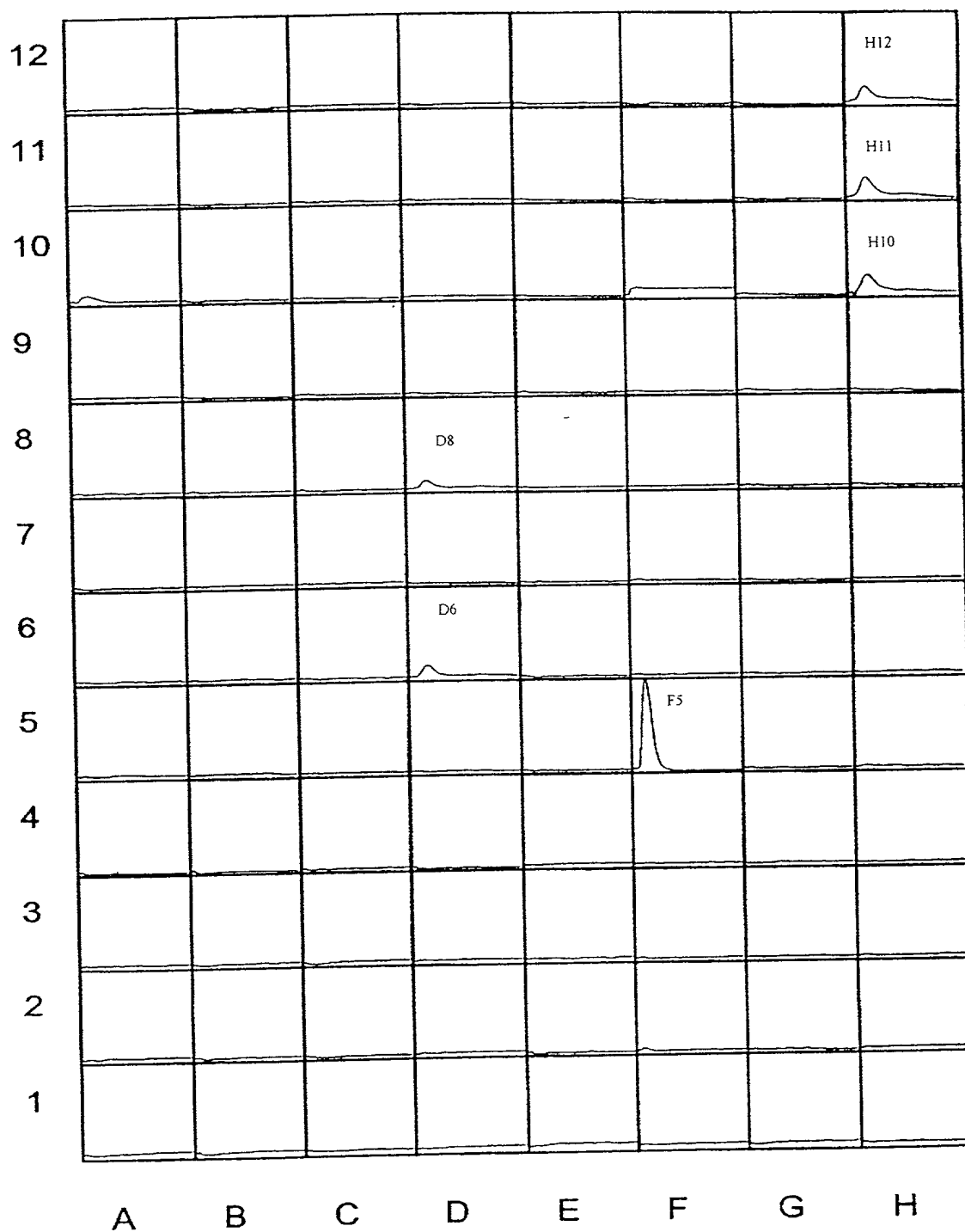
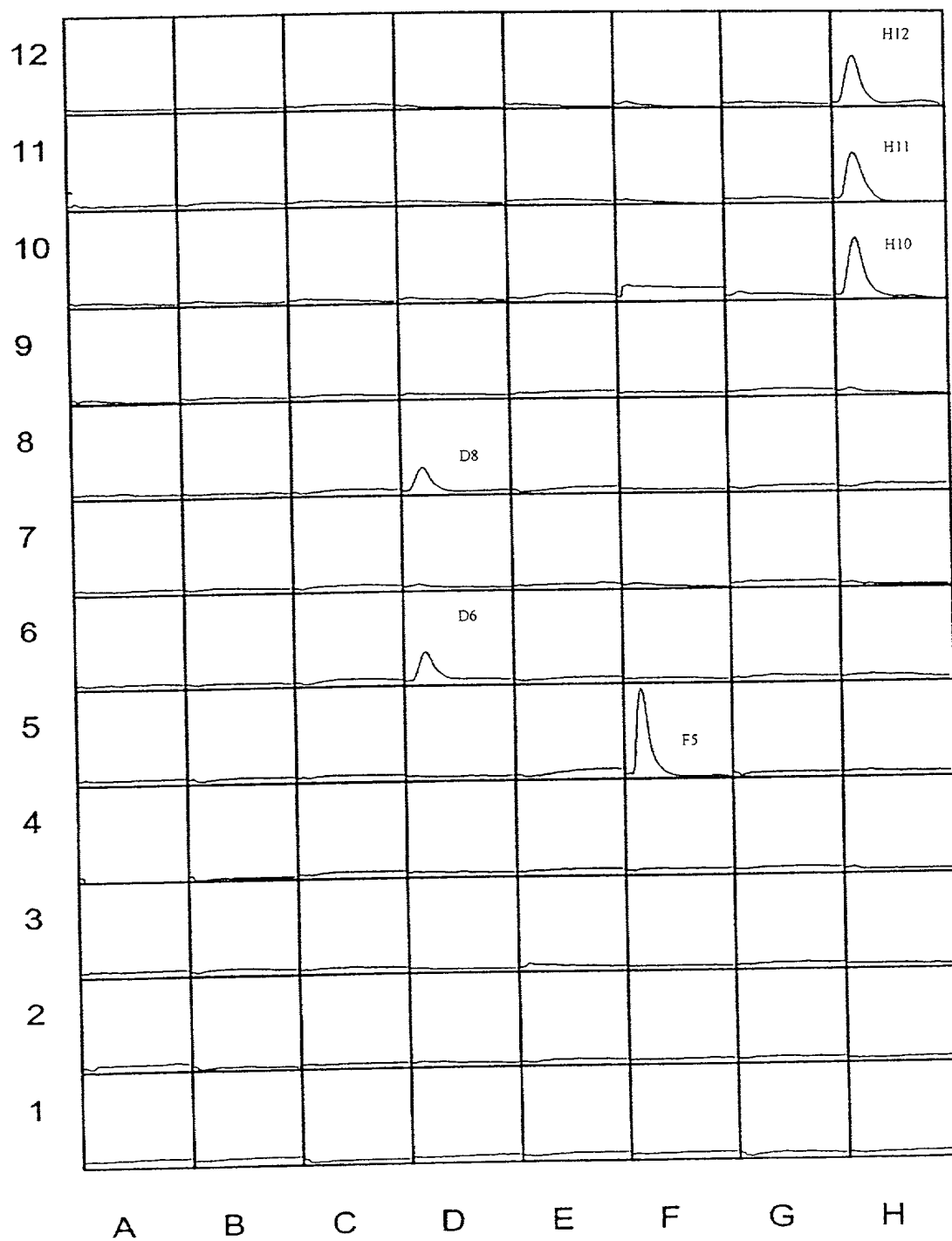


Fig. 7B

hEDG8



Fluorescence change counts

Wells	Lipid	background	hEDG8	stand. response
H10-H12	1µM S1P	3696	9493	5797
F5	1µM LPA	18004	16333	-1671
D8	1µM dhS1P	1683	4522	2839
D6	1µM S1P	2273	5605	3332

Fig. 7C

FIG 8

% S1P response

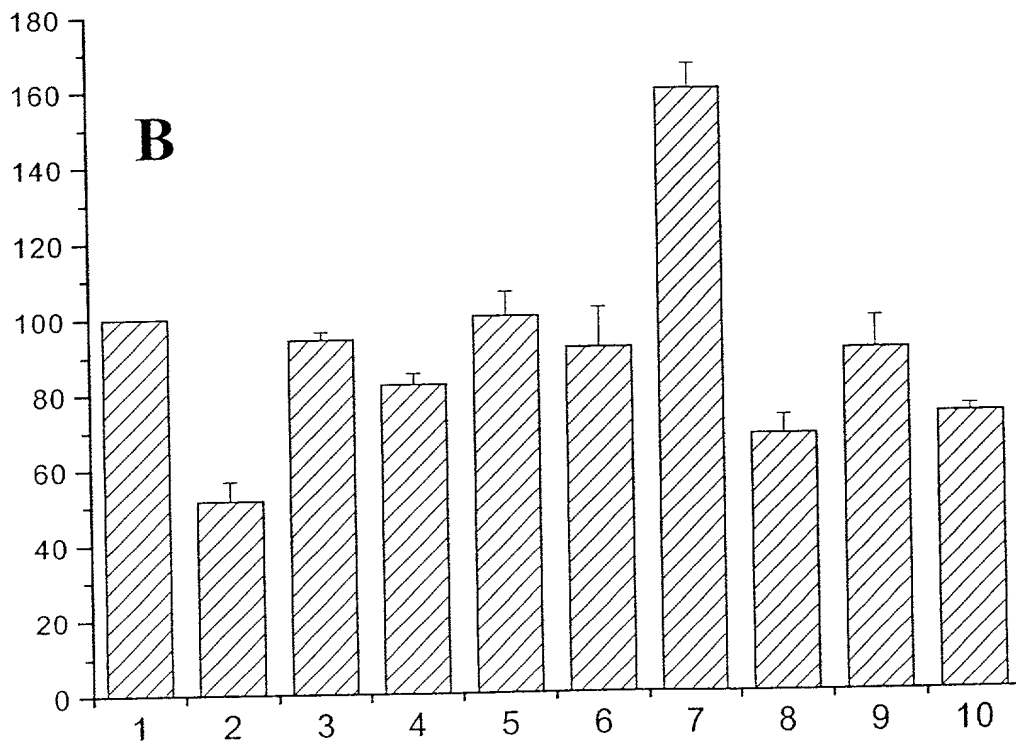
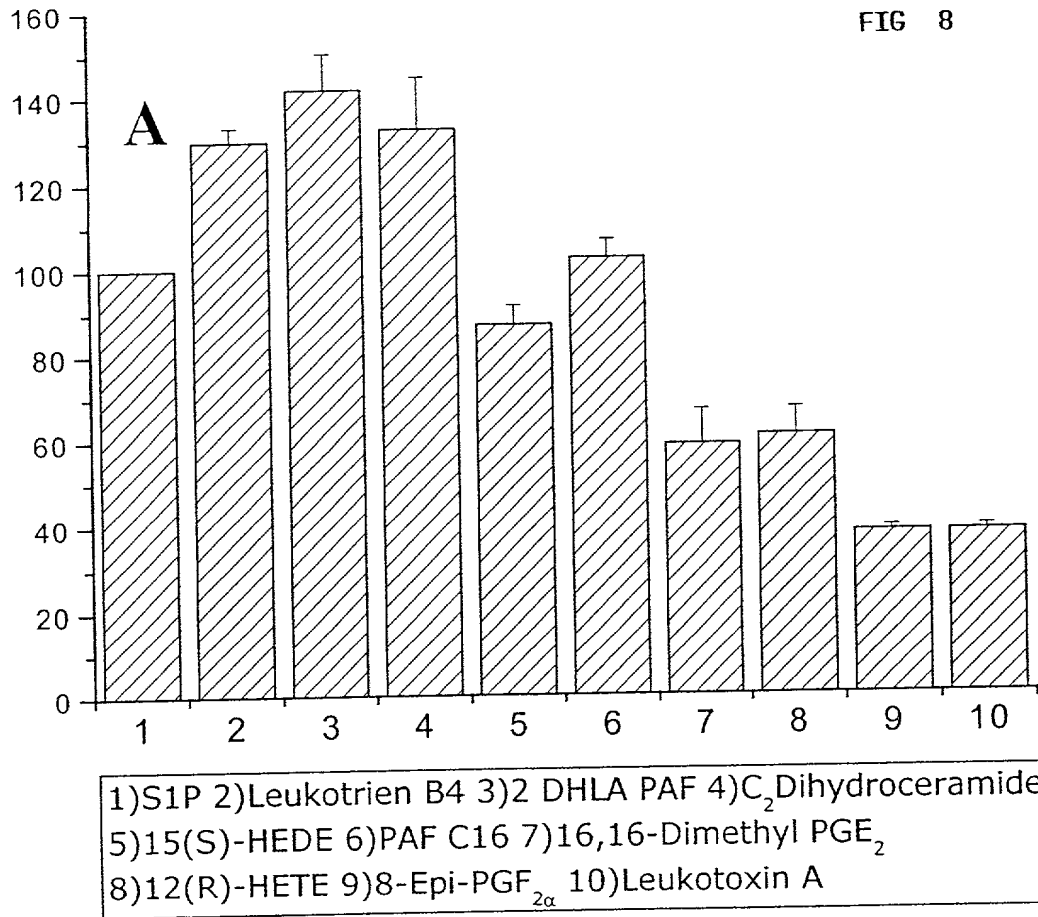
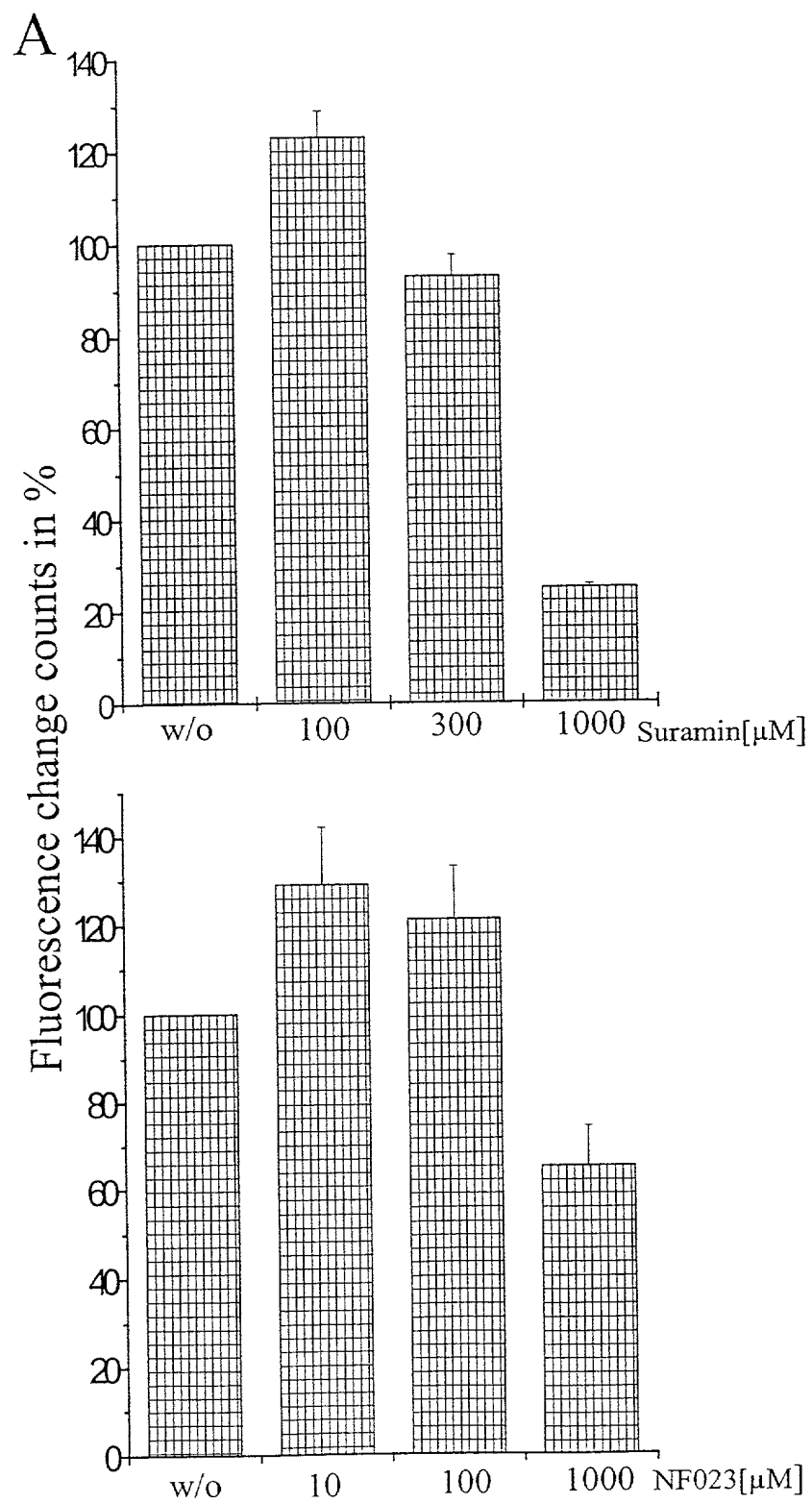


FIG 9A



FTG 9B

